Cancer — unraveling the complexity

Intuitive software

Expedite your understanding of cancer with CLC Cancer Research Workbench

Seeking the meaning of the sequence? Gain valuable insights into cancer with CLC Cancer Research Workbench!

- Quickly analyze complex data
- Modify or personalize analysis workflows
- Conveniently filter and visualize your data
- Compare your results with relevant databases

Sample & Assay Technologies
The truth lurking behind the sequences...

Accelerate next-generation sequencing (NGS) data interpretation and uncover meaningful insights in cancer research with CLC Cancer Research Workbench — the world’s first comprehensive, user-friendly, and customizable cancer-focused informatics solution!

CLC Cancer Research Workbench provides you with all the tools you need to:

- Discover prognostic markers
- Identify subclonal somatic mutations
- Detect inherited traits
- Find biomarkers for drug response
- Determine new oncogenes

Comprehensive analysis so you don’t miss a single detail!

To perform comprehensive cancer data analysis, CLC Cancer Research Workbench offers specialized tools that allow you to:

- Remove germline variants
- Identify rare subclonal mutations and mutated genes for further analysis
- Annotate identified variants with information from COSMIC and ClinVar
- Test the presence of specific variants
- Compare samples and identify new biomarkers

Compare and share your data

Inspect identified variants in the context of mapped sequencing reads, human genes, and relevant variants in clinical databases, including:

- Human genome
- dbSNP
- dbSNP common from UCSC
- COSMIC
- ClinVar
- HapMap
- 1000 genomes data
- Ensembl genes

The intuitive software interface allows you to customize workflows or create new ones. You can also easily share workflows with your collaborators and colleagues (Figures 1–2)!
End-to-end workflows for analysis of cancer data

Whether it is targeted amplicon, exome, or whole genome sequencing data, CLC Cancer Research Workbench is compatible with data generated using all sequencing platforms. From identifying known and novel variants to uncovering somatic variants, as well as annotating your variants with information from databases, amino acid changes, and conservation scores — versatile CLC Cancer Research Workbench provides comprehensive analysis to help you uncover all the details!

Figure 1. Flexible, cancer-specific, ready-to-use workflows.
Analyze results and customize analysis workflows

Results can be explored further using additional tools from the toolbox, and analysis workflows can be customized accordingly.

Figure 2. Build your own customized analysis workflows. With CLC Cancer Research Workbench, you can drag and drop a workflow in the workflow editor, edit it, and install it again, or share workflows with your collaborators and colleagues.

A plugin that includes ready-to-use specific workflows for QIAGEN® Gene Panels is available.

It’s also possible to integrate CLC Cancer Research Workbench with Ingenuity Variant Analysis™. CLC Cancer Research Workbench is part of the CLC Enterprise Platform with support for client-server setup, grid support, and command-line tools. CLC Cancer Research Workbench runs on Mac® OS X, Windows®, and Linux platforms.

Ordering Information

<table>
<thead>
<tr>
<th>Product</th>
<th>Contents</th>
<th>Cat. no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLC Cancer Research Workbench</td>
<td>User-friendly desktop software for next-generation sequencing data analysis for cancer research</td>
<td>Inquire</td>
</tr>
</tbody>
</table>

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Find out more at www.qiagen.com/CLCCancerResearch.